

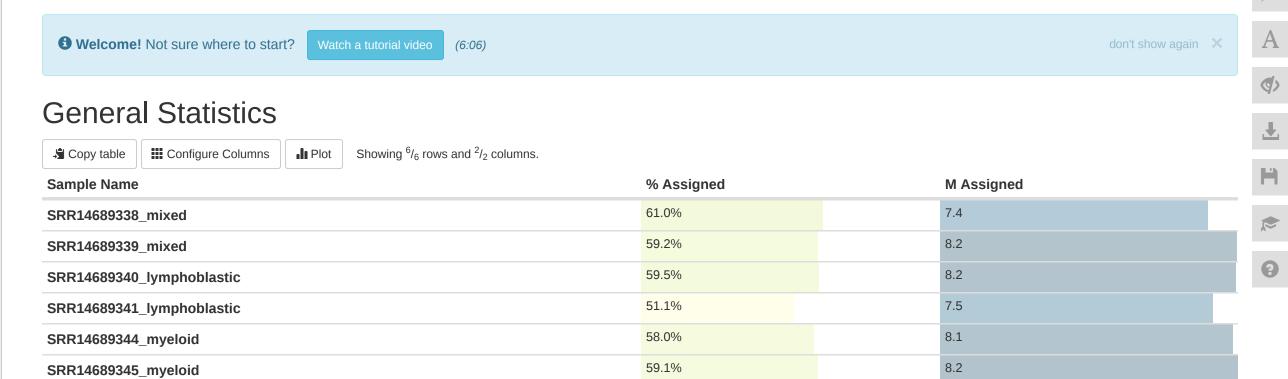
**General Stats** 

featureCounts



A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

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## featureCounts

Subread featureCounts is a highly efficient general-purpose read summarization program that counts mapped reads for genomic features such as genes, exons, promoter, gene bodies, genomic bins and chromosomal locations. DOI: 10.1093/bioinformatics/btt656.

